

Supporting Information

A revertible, autonomous, self-assembled DNA-origami nanoactuator.

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Figure S1. Folding path of the DNA-Origami switch.

The scaffold strand (in blue) is folded with the staple strands starting from the first row on the top. The unfolded nucleotides are indicated with an 'X' on the scaffold. The colors of the staple strand in this image are coherent with the oligonucleotides colors in Supplementary Table 1.

Figure S2. Preliminary check of the well formed structures. The assembly reactions of the DNA switch were run on a standard agarose gel GelRed™ stained and imaged under UV light. 1) 1kb DNA ladder. 2) M13mp18 DNA, used as negative control. 3) DNA origami: besides the band corresponding to the evident excess of staple strands there is only a single sharp band, migrating slower than the M13 DNA.

Figure S3. AFM image of closed (not actuated) DNA origami on freshly cleaved mica surface.

Figure S4. AFM imaging of actuated DNA origami structures. Two high resolution AFM images of a DNA origami, after the addition of the target. In this image the honeycomb structure originated by the alternate coiling of the short staples with the long scaffold typical of DNA origami, is clearly observed. The two images of the same origami are acquired with scan direction rotated of 90deg to each other to rule out possible artifacts in image interpretation.

Figure S5. Additional AFM imaging of DNA origami structures. DNA origami actuated by addition of the target imaged at different magnifications.

Table S1. Oligonucleotides sequences used for the synthesis of the origami.

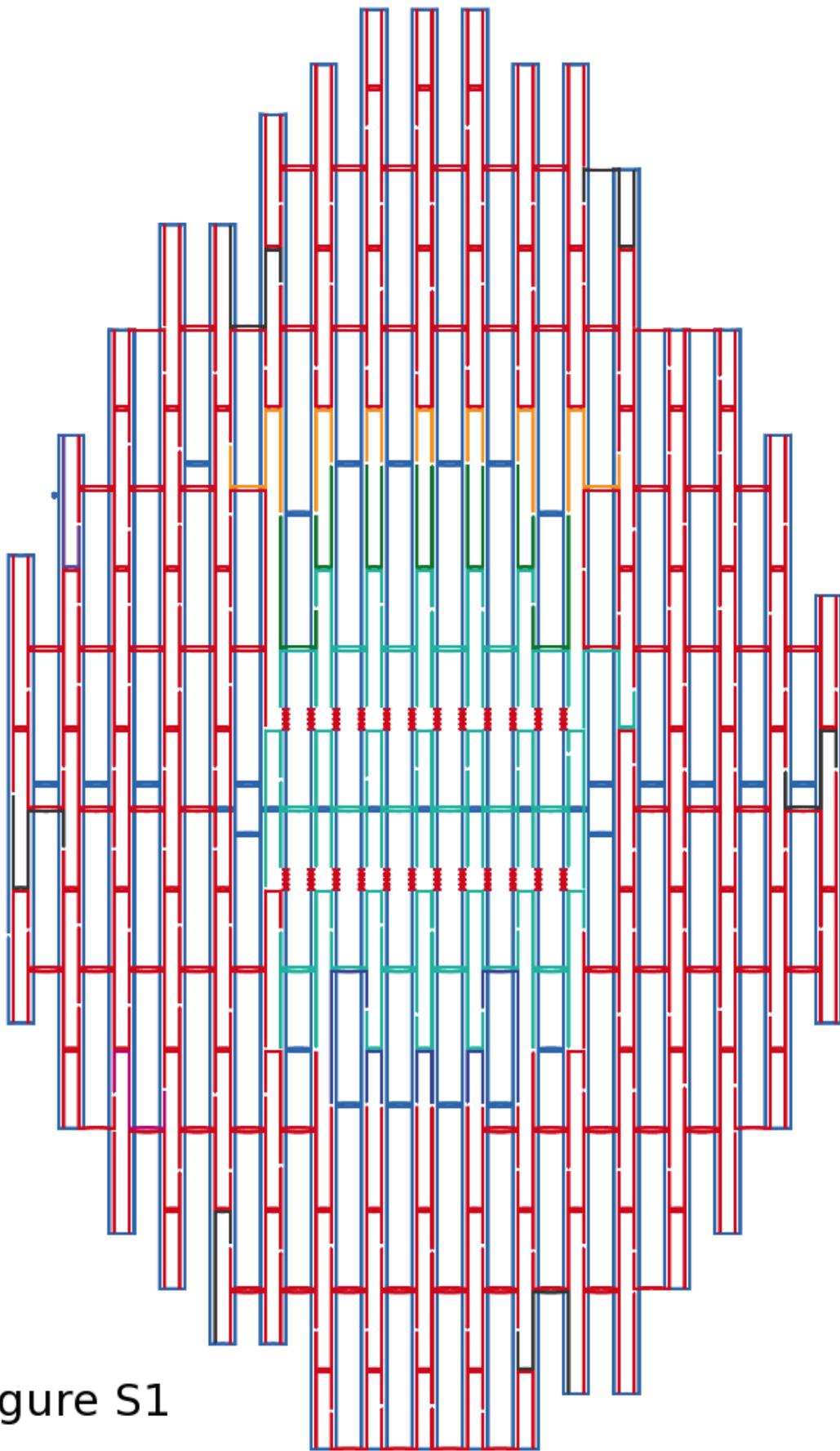


Figure S1

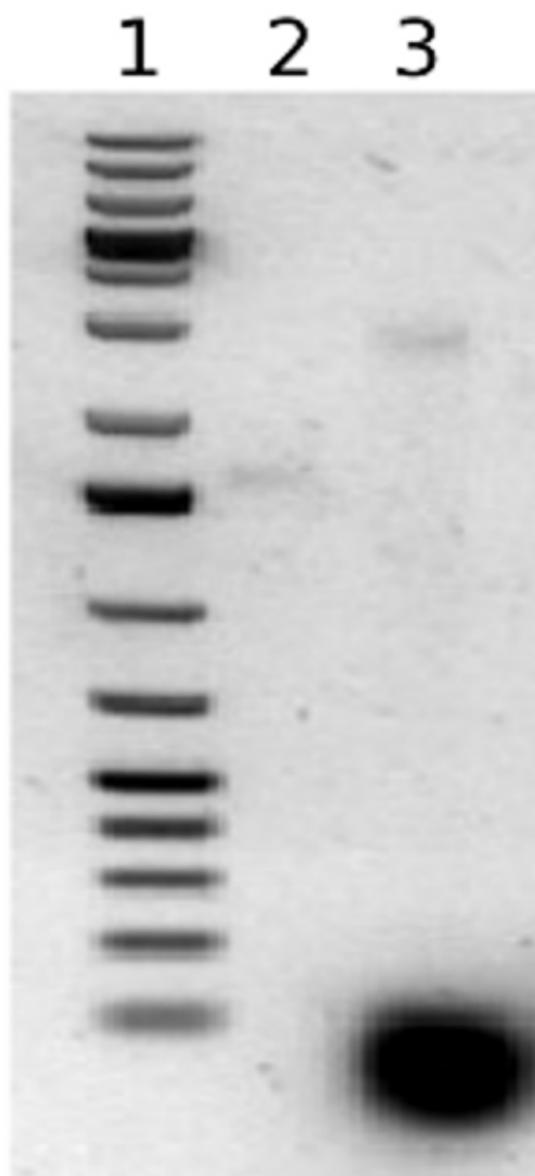


Figure S2

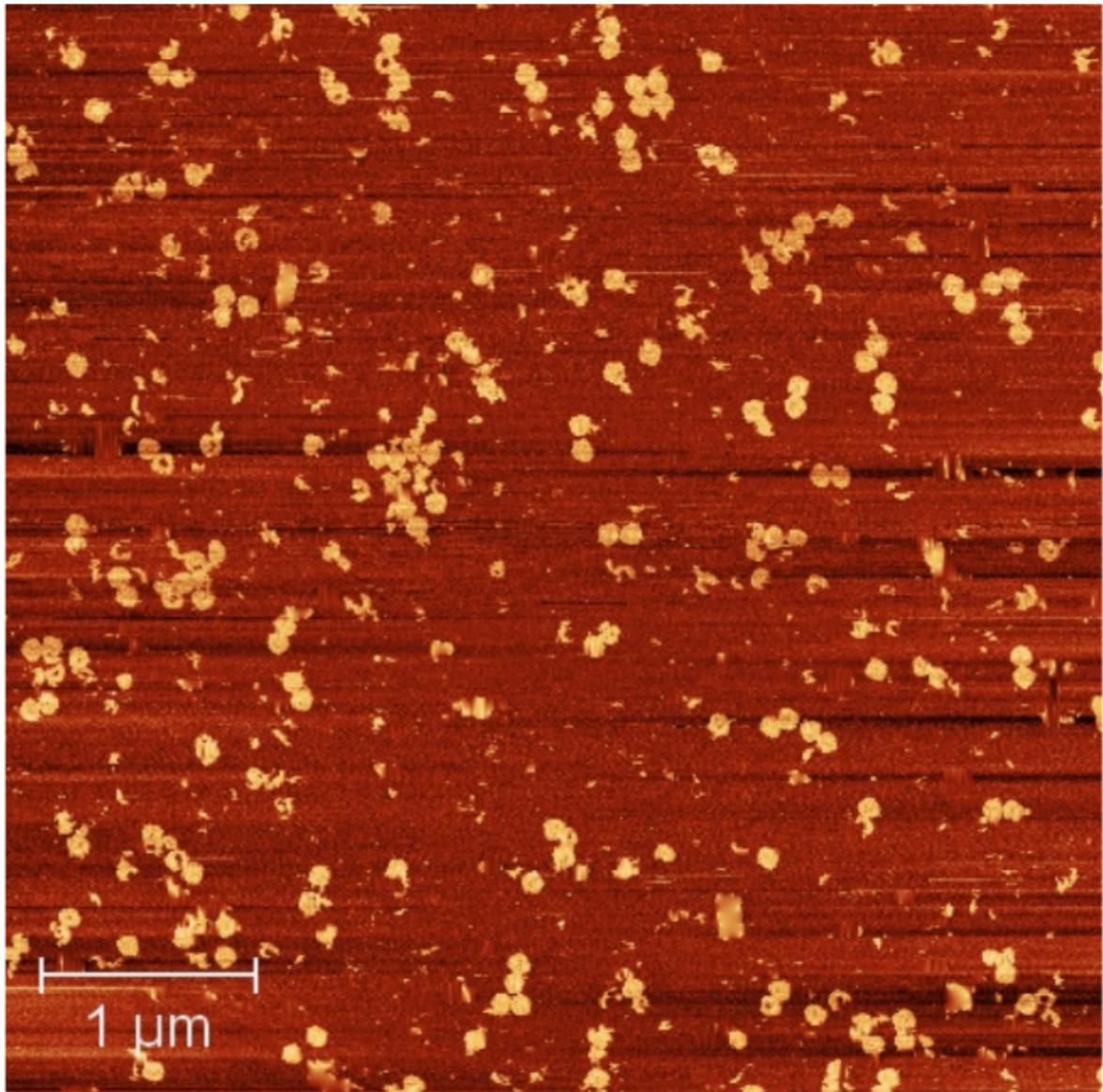


Figure S3

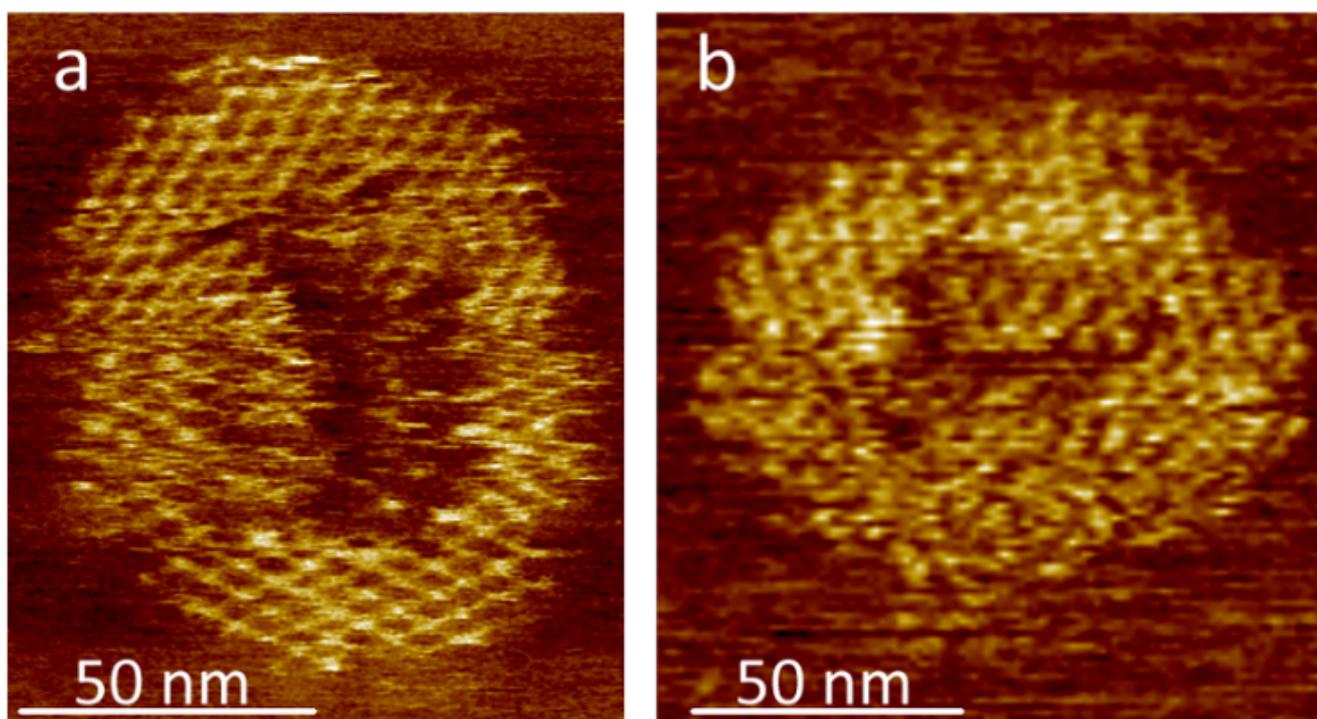


Figure S4

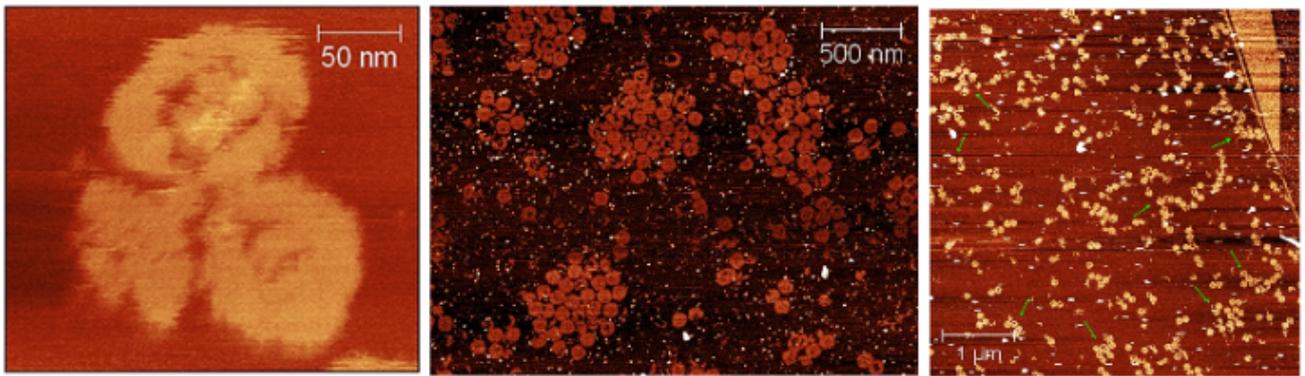


Figure S5

Supplementary Table 1. Oligonucleotides sequences

All the substitutions are intended referred to the standard origami

Standard DNA Origami

Yellow: Oligonucleotides on the internal right edge of the external ring

Grey: External oligonucleotide of the external edges of the ring

Blue: Oligonucleotides on the left edge of the internal disk

Dark Green: Oligonucleotides on the right edge of the internal disk

Light blue: Oligonucleotides of the internal disk

Red: Oligonucleotides of the ring

Sequence	Length	Description	Color
AGGAACGCCATCAAAAATAATGTGTAGATGGGCGCATGCCATTCAG	46	Cr1	Yellow
GATGAACGGTATCAGCTCATTTTTTAACCAAT	32	Cr12	
CCTGAGTAATGACAAGAGAATC	22	Cr13	
CATCCAATAAATAAATGCAATG	22	Cr14	
TAAAGTACGGTAGTAGCATTAA	22	Cr15	
CGCGTTTTAATTCGAGCTTCAAAATATGCAAC	32	Cr16	
GTAAGAGCAATACTGCGGAATCGAGCCCGAAAGACTTCAAATAT	44	Cr17	
TTGTTCCAGTTTGAACAAGAGTCCACTATTAAGTAAATCAA	43	Cr1	Red
AAAGCCGGCGACGCGTAACCACCACACTACTATGGT	36	Cr2	
AGAAAGGACGTCTATCAATTTAGAGCTTGACGGGG	35	Cr3	
AAGAATAGCTGTTTGATGGTGGTTTTTTCACCA	33	Cr4	
CTGGCAAGTGCTTTCCTCGTTAGAGAGCTAAA	32	Cr5	
GGCGGGCGGGAGCAAAATCCCTTAAACGTGGACTCCA	37	Cr6	
TGCTTTGAGACAGGAACGGTACGCGTTGTAGC	32	Cr7	
TATAACGTGTAGCGGTCACGCTGACGTGGCG	31	Cr8	
GTGAGACAGAGGCGGTTTTCGTAATACGAGCC	32	Cr9	
CTGATTGCCAGCAGGCGAAAATCCCCGAGATAGGGTTGAGTG	42	Cr10	
GCCTGGCAGCTGCATTAATGAATGGGTGCCT	31	Cr11	
TGTTTTTATAATCAGTGAGGC	21	Cr12	
TGAGAAGGCCGCTACAGGGCGCGCCGCGCTTAATGCTTTT	39	Cr13	
CAGGAGGCCATCACTTGCCTGAGTAACTATC	32	Cr14	
CAGAGCGGATCAGGGTGGTTTTTCCCGAAATC	32	Cr15	
GCCCCGTTTTCCAGTCGTTGCGTTGCGCTCACTAGGTCGACT	41	Cr16	
CACCGAGTAAAAGAGTCTGTCCGCTCATGGAAATACCTATTTACA	45	Cr17	
AATACTTAATATTACCGCCAGCCCCAGTAATA	32	Cr18	
AGTAATAACGATTAAGGGATTTTACGAGCACG	33	Cr19	
GGAAGCACTGTGTGAAATTGTTATACGTGGC	31	Cr20	
AAGCCTGCGGCCAACGCGCGGGGGGGCAACAG	32	Cr21	
AATGAGTGCTCGAATTCGTAATCATTAGTCTTT	33	Cr22	
ACATTAAGGAAACCTGTGCTGCCCTGAGAGAGT	34	Cr23	
AGGAAAAACATCACGCAAATTAACCCAGAATCC	33	Cr24	
GGCCTTGCGATAGAACCCTTCTGACAATCAAT	32	Cr25	
CAAACCTCAGAAGTTCCACACAACCTGGGCGC	32	Cr26	
CTAGAGGGGGTTTTCCAGTCACGGGGATGTG	32	Cr27	
GTGCCAAGCTTGCATGCCTGC	21	Cr28	
ATCGTCTGAAATGGATTACATTTTGACGCTCA	32	Cr29	
TTGGCAGACATCGAGAACAAGCAAAGATATAG	32	Cr30	
AAAGGGACCAAGAACGGGTATTACGCGAGGC	31	Cr31	
CAACAGATGGTAATATCCAGAACCTTTGATT	31	Cr32	
ACAGACAAAACCACCAGCAGAAGAGCTTTCCGG	33	Cr33	

ATGGCTATGGTCATAGCTGTTTCTAAAGTGTA	32	Cr34
AATGCGCCCCTAAAACATCGCCAAGGCAAAGCGC	34	Cr35
TAACGCCAATCCCCGGGTACCGAGAGCTAACTC	33	Cr36
CCGCACTTTCACCAGTCACACGAATTGCAAC	31	Cr37
AATCGGCTGGGAGGTTTTGGAAACCGGTCCACTCCAGCCATAAAACAG	48	Cr38
AGGTGAGGCCTGAAAGCGTAAGAATCCGCTCA	32	Cr39
CTGCAAGAACTGTTGGGAAGGGCGGGATAGG	31	Cr40
TATTACGCCAGCTGGCGAAAGGACGTTGTA AACGACGGCCATTTT	42	Cr41
ATTACCGCGCCAATTTGCCAGTTTTT	22	Cr42
AAGGCTTATACCAACGCTAACGAGCCCAATCCA	33	Cr43
GTTTTAGCTTTGCACCCAGCTACA	24	Cr44
GACTTGCGTCTTTCTTATCATTCTATTCTGGC	32	Cr45
CACCGCTACGACAGTATCGGCCT	23	Cr46
CGGAAACCTTAAAAATACCGAACGTATTTTTGA	33	Cr47
CATTCCGTAACCGTGCATCTGCCAGTTTGAGGGGACGTCTGGTGC	45	Cr48
GCTGCGCGCGATTAAGTTGATAGGAACTGGG	31	Cr49
TGAATCTTCCGGTATTCTAAGAAAACCAAGTA	32	Cr50
TCACGTTGTGCGCTCTGGCCTTCTTAAATTT	32	Cr51
CCGTCGGATTCTCCGTGGGAACAAACGCAACATTAA	36	Cr52
TACAAAATAAACAGGGAAG	19	Cr53
TTATTTATCGTCTTTCCAGAGCCTCAATAGCAA	33	Cr54
AATAAGATAGCAGCCTTTACAGAATAACCCACAAGAATTGAGTT	44	Cr55
TCCCATCCCAAGATTAGTTGCTATGAACCTCCC	33	Cr56
ATGTGAGTTGTAACGTTAATATCCGGTTGAT	32	Cr57
CGCATTAGTCAGAGGGTAATTGAGATAGCTAT	32	Cr58
ACGTCAAAAATGAAAAACGATTTTTTTGTTTAAATTTTATCC	41	Cr59
TTGTTAAAATCGTAAACTAGCATTGAGAGTC	32	Cr60
TTGTATAAGCAAATATTTAAACGAGTAACAAC	32	Cr61
GAACAAAGACGGGAGAATTA ACTG	24	Cr62
CAGAGAGGAGAATAACATAAAAAACAGCCATA	31	Cr63
ATGTACCTTTGTTAAAATTCGCATGTAGCCAG	32	Cr64
AATCAGAGAGAGATCTACAAAGGCGGAGACAG	32	Cr65
CTTACCGAAACAAAGTTACCAGAATGTTAGCA	32	Cr66
AAGCCCAATAATAAGAGCAAGCAATAATAACGGAATACCCAA	42	Cr67
TGGAGCAATGTAGGTAAAGATT CAGAACCCTCA	33	Cr68
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ATTATGACCCTGTAATCGGTTGTACCAAAAAC	32	Cr79
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GATTGAGGTTAAAGGTGAATTATCCGGAAACG	32	Cr84
TCATATGGTTTACCAGCGCCAGCCATTTGGGAATTAGATCACCAG	45	Cr85
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GCTATATTGAGCATAAAGCTAAATACTTTTTGC	32	Cr87
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AACCTACCATATCAAAATTATAGAAACAATAACGGATTCGCC	42	DkD5
TGATTGCTTTGAATACCAAGTACATTTAACAA	32	DkD6
TTTCATTTGAATTACCTTTTTTAAATGGGAAAAACAAA	36	DkD7



Probe

5'-

CGATCCGACCTTCCTCCCTCCTCCTCCTTCCCTTGGGTTCGAACATTGCTCGTCGTCACTGG
GTCCTGCTCATATTGGGTTTACAGCTCACATAGGTAGACTTTAGCTTCCCGGGCTCGCA
G-3'

Target

5'-

GGGCGGGGCGGGGGCGCGAAAGTCTACCTATGTGAGCTGTAAACCCAATATGAGCAG
GACCCAGTGACGACGAGCAATGTTTCGACCCAAGGGAAGAGGAGGACGCGCCCCCGCC
CCGCCC-3'

Target mismatch

5'-

GGGCGGGGCGGGGGCGCGAAAGTCTACCTATGTGAGCTGTAAATTTGGCCGAGTTCAA
GTTACTGACGACAAGTTCCTGTTTCGACCCAAGGGAAGAGGAGGACGCGCCCCCGCCCC
CCC-3'

Competitor

5'-

TCCTCCTCCTCCCTTGGGTTCGAACAGGAACTTGTCGTCAGTAACTTGAACCTCGGCCAAA
TTTACAGCTCACATAGGTAGACTTT-3'

To link a probe to the origami

substitute

DkD4 with LinkerDx:

5'-

GGGAGGAAGGTCGGATCGCTACCATCGGAACAAAGAAATCTGAATAATGGAAGGGTT
AG- 3'

DkS3 with Linker Sx

5'- TGGTTTCAAATATACAAATCATGCTGCGAGCCCGGGAAGCT - 3'

For the FRET visualization

substitute

DkD3 with Dk_{FRET}

5'- 6-FAM- TAGAGCCGTCAATTTAAAAGTTTGAGTAACATTA -3'

CrI3 with Cr_{FRET}

5'- CCTGAGTAATGACAAGAGA – BHQ1 -3'